



SEQUENCE LISTING

GENERAL INFORMATION

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<120> TITLE OF INVENTION: Characteristics of Phenylalanine Ammonia-lyase (PAL) Gene in Wounded Lettuce Tissue

<130> FILE REFERENCE: UCDA.004.01US

<140> CURRENT APPLICATION NUMBER: 09/964,992

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<160> NUMBER OF SEQ ID NOS: 5

<170> SOFTWARE: PatentIn version 3.0

<210> SEQ ID NO: 1

<211> LENGTH: 711

<212> TYPE: PRT

<213> ORGANISM Lactuca sativa

<400> SEQUENCE 1

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Lys Asp Pro Leu Asn Trp Gly Val Ala Ala Glu Ala Leu Thr Gly Ser
20          25          30

His Leu Asp Glu Val Lys Lys Met Val Ala Glu Phe Arg Lys Pro Val
35          40          45

Val Lys Leu Gly Gly Glu Thr Leu Thr Val Ser Gln Val Ala Gly Ile
50          55          60

Ala Ala Ala Asn Asp Ser Asp Thr Val Lys Val Glu Leu Ser Glu Ala
65          70          75          80

Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val Met Glu Ser Met
85          90          95

Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly Phe Gly Ala Thr
100         105         110

Ser His Arg Arg Thr Lys Gln Gly Gly Ala Leu Gln Lys Glu Leu Ile
115         120         125

Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr Glu Thr Ser His
130         135         140

Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met Ile Val Arg Ile Asn
145         150         155         160

Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu Ile Leu Glu Ala
165         170         175

Ile Thr Lys Phe Leu Asn Asn Asn Ile Thr Pro Cys Leu Pro Leu Arg
180         185         190

Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu Ser Tyr Ile Ala
195         200         205

Gly Leu Leu Thr Gly Arg Pro Asn Ser Lys Ala Val Gly Pro Thr Gly
210         215         220

Glu Val Leu Asn Ala Glu Lys Ala Phe Ala Ala Ala Gly Val Glu Gly
225         230         235         240

Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly
245         250         255

Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu Phe Asp Ala Asn
260         265         270

Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val
275         280         285

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Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys  
 290 295 300  
 His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu Tyr Ile Leu  
 305 310 315 320  
 Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val His Glu Met Asp  
 325 330 335  
 Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro  
 340 345 350  
 Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser Ser Thr Lys Met  
 355 360 365  
 Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val  
 370 375 380  
 Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile  
 385 390 395 400  
 Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys  
 405 410 415  
 Leu Met Phe Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn  
 420 425 430  
 Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Tyr  
 435 440 445  
 Gly Phe Lys Gly Gly Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu  
 450 455 460  
 Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln  
 465 470 475 480  
 His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr  
 485 490 495  
 Ala Glu Ala Val Asp Ile Leu Lys Leu Met Ser Ser Thr Tyr Leu Val  
 500 505 510  
 Ala Leu Lys Gln Ser Ile Asp Leu Arg His Leu Glu Glu Asn Met Lys  
 515 520 525  
 Ser Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Lys Val Leu Thr  
 530 535 540  
 Met Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp  
 545 550 555 560  
 Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Ile Asp Asp  
 565 570 575  
 Val Lys Ser Gly Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu  
 580 585 590  
 Val Asp His Ala Leu Asn Asn Gly Glu Thr Glu Lys Asn Thr Asn Thr

595                      600                      605  
 Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Glu Glu Leu Lys Val Leu  
 610                      615                      620  
 Leu Pro Lys Glu Val Glu Gly Val Arg Ile Ala Tyr Glu Asn Asp Thr  
 625                      630                      635                      640  
 Leu Ser Ile Pro Asn Arg Ile Lys Ala Cys Arg Ser Tyr Pro Leu Tyr  
 645                      650                      655  
 Arg Phe Val Arg Glu Glu Leu Gly Arg Gly Phe Leu Thr Gly Glu Lys  
 660                      665                      670  
 Val Thr Ser Pro Gly Glu Glu Phe Asp Arg Val Phe Thr Ala Met Cys  
 675                      680                      685  
 Lys Gly Gln Ile Ile Asp Pro Leu Leu Glu Cys Leu Gly Gly Trp Asn  
 690                      695                      700  
 Gly Glu Pro Leu Pro Ile Cys  
 705                      710

<210> SEQUENCE ID NO: 2

<211> LENGTH: 712

<212> TYPE: PRT

<213> ORGANISM: Lactuca sativa

<400> SEQUENCE 2

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 Ala Glu Phe Cys Val Gly Asp Pro Leu Asn Trp Gly Met Ala Ala Glu  
 20                      25                      30  
 Ser Leu Lys Gly Ser His Leu Asp Glu Val Lys Arg Met Val Ala Glu  
 35                      40                      45  
 Phe Arg Lys Pro Val Val Arg Leu Gly Gly Glu Thr Leu Thr Val Ser  
 50                      55                      60  
 Gln Val Ala Ala Ile Ala Ala Ser Asp Asn Ala Gly Val Lys Val Gln  
 65                      70                      75                      80  
 Leu Ser Glu Thr Ala Arg Ala Gly Val Lys Ala Ser Ser Asp Trp Val  
 85                      90                      95  
 Met Glu Ser Met Asn Lys Gly Thr Asp Ser Tyr Gly Val Thr Thr Gly  
 100                      105                      110  
 Ile Gly Ala Thr Ser His Arg Arg Thr Lys Glu Gly Gly Ala Leu Gln  
 115                      120                      125  
 Lys Gln Leu Ile Arg Phe Leu Asn Ala Gly Ile Phe Gly Asn Gly Thr

130	135	140
Glu Ser Thr His Thr Leu Pro His Ser Ala Thr Arg Ala Ala Met Leu		
145	150	155 160
Val Arg Ile Asn Thr Leu Leu Gln Gly Tyr Ser Gly Ile Arg Phe Glu		
	165	170 175
Ile Leu Glu Ala Ile Thr Lys Phe Leu Asn His Asn Val Thr Pro Phe		
	180	185 190
Leu Pro Leu Arg Gly Thr Ile Thr Ala Ser Gly Asp Leu Val Pro Leu		
	195	200 205
Ser Tyr Ile Ala Gly Leu Leu Thr Gly Arg Ala Asn Ser Lys Ala Val		
	210	215 220
Gly Pro Thr Gly Glu Val Leu Asn Ala Glu Lys Ala Phe Ala Glu Ala		
	225	230 235 240
Gly Val Glu Gly Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala		
	245	250 255
Leu Val Asn Gly Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu		
	260	265 270
Phe Asp Ala Asn Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile		
	275	280 285
Phe Ala Glu Val Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr		
	290	295 300
His Lys Leu Lys His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met		
	305	310 315 320
Glu Tyr Ile Leu Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val		
	325	330 335
His Glu Met Asp Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu		
	340	345 350
Arg Thr Ser Pro Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser		
	355	360 365
Ser Thr Lys Met Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro		
	370	375 380
Leu Ile Asp Val Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln		
	385	390 395 400
Gly Thr Pro Ile Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala		
	405	410 415
Ala Ile Gly Lys Leu Met Phe Ala Gln Phe Ser His Leu Val Asn Asp		
	420	425 430
Phe Tyr Asn Asn Gly Leu Pro Ser Asn Leu Ser Gly Gly Arg Asn Ile		
	435	440 445

Ser Leu Asp Tyr Gly Phe Lys Gly Ala Glu Ile Ala Met Ala Ser Tyr  
 450 455 460  
 Cys Ser Glu Leu Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln  
 465 470 475 480  
 Ser Ala Glu Gln His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser  
 485 490 495  
 Ala Arg Lys Thr Ala Glu Ser Val Glu Ile Leu Lys Leu Met Ser Thr  
 500 505 510  
 Thr Tyr Leu Val Ala Leu Cys Gln Ser Ile Asp Leu Arg His Leu Glu  
 515 520 525  
 Glu Asn Leu Lys Ser Thr Val Lys Asn Thr Val Ser Leu Val Ala Lys  
 530 535 540  
 Lys Ile Leu Thr Thr Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe  
 545 550 555 560  
 Cys Glu Lys Asp Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala  
 565 570 575  
 Tyr Ile Asp Asp Ala Cys Ser Ala Thr Tyr Pro Leu Met Gln Lys Leu  
 580 585 590  
 Arg Gln Val Ile Val Asp His Ala Leu Asn Asn Glu Asn Asp Ala Gly  
 595 600 605  
 Thr Ser Ile Phe Gln Lys Ile Ser Glu Phe Glu Glu Glu Leu Lys Ala  
 610 615 620  
 Val Leu Pro Lys Glu Val Glu Gly Val Arg Ser Ala Tyr Glu Ser Ser  
 625 630 635 640  
 Thr Leu Thr Ile Pro Asn Arg Ile Lys Glu Cys Arg Ser Tyr Pro Leu  
 645 650 655  
 Tyr Arg Phe Val Arg Glu Glu Leu Gly Thr Gly Phe Leu Thr Gly Glu  
 660 665 670  
 Glu Val Thr Ser Pro Gly Glu Glu Phe Asp Lys Val Phe Thr Ala Leu  
 675 680 685  
 Lys Lys Gly His Ile Ile Asp Pro Leu Leu Glu Cys Val Gln Gly Trp  
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 Asn Gly Val Pro Leu Pro Ile Ser  
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-210- SEQ ID NO 3

-211- LENGTH 2442

-212- TYPE cDNA

<213> ORGANISM: Lactuca sativa

(400) SEQUENCE 3

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ggagaacggt aatcacgtta atggagtcgt taatgaggtg tgpaccaagg atccattgaa    180
ctggggaggt ggaggggagg cgttgacggg aagtcacctt gatgaggtga agaagatggt    240
tggggagtto agaaagcggg tggggaagct cggaggagag acgcttacag tttctcaggt    300
gggggggata gtagctgcta atgacagtga caccgtgaag gtggagctgt cggaagccgc    360
gagggctgga gtaagggcga gtagtgattg ggttatggag agcatgaata aaggaactga    420
tagttatggt gtcaccacgg gcttcggcgc caccctccac cggagaacta agcaaggcgg    480
ccctttacag aaggagctca ttagattttt gaacgcggga atattcggca atggaacgga    540
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ctcctccacg ggtaactccg gcctccgatt cgagatcttg gaagccatca ccaagttcct    660
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gttcttcgag ttacggcgca aagaagggtt agcaatttgt aagggaaccg cgtgggggtt    900
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ggctctcacc atgggcgtca acggcgagct ccacccgtcg agattctggg agaaagatct 1800  
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gaaagtctctg ttaccgaaaag aagtccaagg tcttagaatt gcttatgaga atgatacatt 2040  
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<210> SEQ ID NO: 4

<211> LENGTH: 2380

<212> TYPE: cDNA

<213> ORGANISM: Lactuca sativa

<400> SEQUENCE 4

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gagagggag tctgtgtga aaggggatcc ttggaattgg gggatggggg cggagtcatt 180  
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gatcccgccc atccggaagc taatgttcgc tcagttctct gagcttctca acgattttta 1380  
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ctttctttta caaattttt tcatgaattt cgaggatttt gtaattgga actcttattt 2280

caaatgtgta tgtaattgta atgtactatt gtatgtttgt aattgtacca cgttaagtgt 2340  
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<210> SEQ ID NO: 5

<211> LENGTH: 666

<212> TYPE: PRT

<213> ORGANISM: Common Sunflower (Helianthus annuus)

<400> SEQUENCE 5

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			20					25					30			
His	Leu	Asp	Glu	Val	Lys	Lys	Met	Val	Gly	Glu	Phe	Arg	Lys	Pro	Val	
			35				40					45				
Val	Lys	Leu	Gly	Gly	Glu	Thr	Leu	Thr	Val	Ser	Gln	Val	Ala	Gly	Ile	
			50				55					60				
Ser	Ala	Ala	Gly	Asp	Gly	Asn	Met	Val	Lys	Val	Glu	Leu	Ser	Glu	Ala	
						70				75				80		
Ala	Arg	Ala	Gly	Val	Lys	Ala	Ser	Ser	Asp	Trp	Val	Met	Glu	Ser	Met	
						85				90				95		
Asn	Lys	Gly	Thr	Asp	Ser	Tyr	Gly	Val	Thr	Thr	Gly	Phe	Gly	Ala	Thr	
			100					105					110			
Ser	His	Arg	Arg	Thr	Lys	Asn	Gly	Gly	Ala	Leu	Gln	Lys	Glu	Leu	Ile	
			115					120				125				
Arg	Phe	Leu	Asn	Ala	Gly	Ile	Phe	Gly	Asn	Gly	Thr	Glu	Ser	Ser	His	
			130					135				140				
Thr	Leu	Pro	His	Ser	Ala	Thr	Arg	Ala	Ala	Met	Ile	Val	Arg	Ile	Asn	
			145			150				155				160		
Thr	Leu	Leu	Gln	Gly	Tyr	Ser	Gly	Ile	Arg	Phe	Glu	Ile	Leu	Glu	Ala	
				165				170					175			
Ile	Thr	Lys	Phe	Leu	Asn	Asn	Asn	Ile	Thr	Pro	Cys	Leu	Pro	Leu	Arg	
				180				185				190				
Gly	Tar	Ile	Thr	Ala	Ser	Gly	Asp	Leu	Val	Pro	Leu	Ser	Tyr	Ile	Ala	
				195			200					205				
Gly	Leu	Leu	Thr	Gly	Arg	Pro	Asn	Ser	Lys	Ala	Val	Gly	Pro	Ala	Gly	
				210			215					220				
Gln	Val	Leu	Asn	Ala	Glu	Ser	Ala	Ile	Ala	Gln	Ala	Gly	Val	Gln	Gly	

225		230		235		240
Gly Phe Phe Glu Leu Gln Pro Lys Glu Gly Leu Ala Leu Val Asn Gly						
	245			250		255
Thr Ala Val Gly Ser Gly Met Ala Ser Met Val Leu Phe Glu Ala Asn						
	260			265		270
Val Leu Ala Leu Leu Ser Glu Val Leu Ser Ala Ile Phe Ala Glu Val						
	275			280		285
Met Gln Gly Lys Pro Glu Phe Thr Asp His Leu Thr His Lys Leu Lys						
	290			295		300
His His Pro Gly Gln Ile Glu Ala Ala Ala Ile Met Glu Tyr Ile Leu						
	305			310		315
Asp Gly Ser Asp Tyr Val Lys Ala Ala Gln Lys Val His Glu Met Asp						
	325			330		335
Pro Leu Gln Lys Pro Lys Gln Asp Arg Tyr Ala Leu Arg Thr Ser Pro						
	340			345		350
Gln Trp Leu Gly Pro Gln Ile Glu Val Ile Arg Ser Ala Thr Lys Met						
	355			360		365
Ile Glu Arg Glu Ile Asn Ser Val Asn Asp Asn Pro Leu Ile Asp Val						
	370			375		380
Ser Arg Asn Lys Ala Leu His Gly Gly Asn Phe Gln Gly Thr Pro Ile						
	385			390		395
Gly Val Ser Met Asp Asn Thr Arg Leu Ala Ile Ala Ala Ile Gly Lys						
	405			410		415
Val Thr Ile Ala Gln Phe Ser Glu Leu Val Asn Asp Phe Tyr Asn Asn						
	420			425		430
Gly Leu Pro Ser His Leu Ser Gly Gly Arg Asn Pro Ser Leu Asp Ser						
	435			440		445
Gly Phe Lys Gly Gly Glu Ile Ala Met Ala Ser Tyr Cys Ser Glu Leu						
	450			455		460
Gln Phe Leu Ala Asn Pro Val Thr Asn His Val Gln Ser Ala Glu Gln						
	465			470		475
His Asn Gln Asp Val Asn Ser Leu Gly Leu Ile Ser Ala Arg Lys Thr						
	485			490		495
Ala Glu Ala Val Asp Ile Leu Lys Leu Met Ser Ser Thr Tyr Leu Val						
	500			505		510
Ala Leu Cys Gln Ser Ile Asp Leu Arg His Leu Glu Glu Asn Met Lys						
	515			520		525
Val Thr Val Lys Asn Thr Val Ser Gln Val Ala Lys Lys Val Leu Thr						
	530			535		540

Met Gly Val Asn Gly Glu Leu His Pro Ser Arg Phe Cys Glu Lys Asp  
 545 550 555 560  
 Leu Leu Arg Val Val Asp Arg Glu Tyr Val Phe Ala Tyr Ala Asp Asp  
 565 570 575  
 Pro Cys Leu Thr Thr Tyr Pro Leu Met Gln Lys Leu Arg Gln Val Leu  
 580 585 590  
 Val Asp His Ala Leu Asn Asn Gly Glu Thr Glu Lys Asn Ala Asn Thr  
 595 600 605  
 Ser Ile Phe Gln Lys Ile Ala Thr Phe Glu Asp Glu Leu Lys Ala Ile  
 610 615 620  
 Leu Pro Lys Glu Val Glu Ser Val Arg Val Ala Phe Glu Asn Gly Thr  
 625 630 635 640  
 Met Ser Ile Pro Asn Arg Ile Lys Ala Cys Arg Ser Tyr Pro Leu Tyr  
 645 650 655  
 Arg Phe Val Arg Glu Glu Leu Gly Gly Ala  
 660 665